

G. BAGAIISKY

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TECH CENTER 1600/2900

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/403,861A

DATE: 01/08/2001  
TIME: 15:12:03

Input Set : A:\Riccardi1.txt  
Output Set: N:\CRF3\01082001\I403861A.raw

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SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: RICCARDI, Carlo  
8 (ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL  
9 DEATH PATHWAYS

11 (iii) NUMBER OF SEQUENCES: 15

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
15 (B) STREET: 624 Ninth Street, N.W., Suite 300  
16 (C) CITY: Washington  
17 (D) STATE: D.C.  
18 (E) COUNTRY: USA  
19 (F) ZIP: 20001

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

28 (A) APPLICATION NUMBER: US/09/403,861A  
29 (B) FILING DATE: 11-Feb-2000

C--> 35 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: PCT/EP98/02490  
33 (B) FILING DATE: 27-APR-1998  
36 (A) APPLICATION NUMBER: EP 97107033.9  
37 (B) FILING DATE: 28-APR-1997

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: YUN, Allen C.  
41 (B) REGISTRATION NUMBER: 37,971  
42 (C) REFERENCE/DOCKET NUMBER: RICCARDI-1

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 202-628-5197  
46 (B) TELEFAX: 202-737-3528

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1972 base pairs  
53 (B) TYPE: nucleic acid  
54 (C) STRANDEDNESS: single  
55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

59 (iii) HYPOTHETICAL: NO

61 (iv) ANTI-SENSE: NO

63 (ix) FEATURE:

64 (A) NAME/KEY: CDS

C--> 65 (B) LOCATION: 206..616

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

69 CTGGCTGCTG TGGAGTTTGT GACATACTAG GTGACACCCCT TGGAGTCACT TCTCTTCAAC

60

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71	TCCAGCTTAG	AAGTGCCTGC	CTGGCTCAGG	GTC TGC ACTG	CAGCCTACTC	CTTGCTTCAG	120
73	CGCCTGACTG	CAACCCAAA	GCCTATCCTA	TACCGCCAGC	CCAGCAGCC	ACTCAAACCA	180
75	GCCACAGCTC	CCCGGCAACC	GAACC	ATG AAC ACC	GAA ATG TAT	CAG ACC CCC	232
76	Met Asn Thr Glu Met Tyr Glu Thr Pro						
77	1	5					
79	ATG GAG	GTG GCC	GTC TAT	CAG CTG CAC	AAT TTC	TCC ACC TCC	280
80	Met Glu	Val Ala	Val Tyr	Gl Glu Leu	His Asn Phe	Ser Thr Ser Phe	
81	10	15	20			25	
83	TCT TCT	CTG CTT	GCA CGG	GAT GTG GTT	TCC GTT AAA	CTG GAT AAC AGT	328
84	Ser Ser	Leu Leu	Gly Gly	Asp Val Val	Ser Val Lys	Leu Asp Asn Ser	
85	30	35	40				
87	GCC TCC	GGA GCC	AGT GTG GTG	GCC CTA	GAC AAC AAG	ATT GAG CAG	376
88	Ala Ser	Gly Ala	Ser Val Val	Ala Leu Asp	Asn Lys Ile	Glu Gln Ala	
89	45	50	55				
91	ATG GAC	CTC GTG	AAG AAC	CAC CTG ATG	TAC GCT GTG	AGA GAG GAG	424
92	Met Asp	Leu Val	Lys Asn	His Leu Met	Tyr Ala Val	Arg Glu Glu Val	
93	60	65	70				
95	GAG GTC	CTA AAG	GAG CAG	ATT CCT GAG	CTG CTT GAG	AAG AAC TCC CAG	472
96	Glu Val	Leu Lys	Glu Gln Ile	Arg Glu Leu	Leu Glu Lys	Asn Ser Gln	
97	75	80	85				
99	CTG GAG	CGC GAG	AAC ACC	CTC CTG AAG	ACG CTG GCA	AGC CCC GAG CAA	520
100	Leu Glu	Arg Glu	Asn Thr	Leu Leu Lys	Thr Leu Ala	Ser Pro Glu Gln	
101	90	95	100			105	
103	CTG GAA	AAG TTC	CAG TCC	CGG CTG AGC	CCT GAA GAG	CCA GCA CCT GAA	568
104	Leu Glu	Lys Phe	Gln Ser	Arg Leu Ser	Pro Glu Glu	Pro Ala Pro Glu	
105	110	115	120				
107	GCC CCA	GAA ACC	CCG GAA ACC	CCG GAA GCC	CCT GGT GGT	TCT GCG GTG	616
108	Ala Pro	Glu Thr	Pro Glu	Thr Pro Glu	Ala Pro	Gly Gly Ser Ala Val	
109	125	130	135				
111	TAAGTGGCTC	TGTCCTTAGG	GTGGGCAGAG	CCACATCTTG	TTCTACCTAG	TTCTTTCCAG	676
113	TTTGTGTTTC	GCTCCCCAAG	GGTCATCTCA	TGTGGAGAAC	TTTACACCTA	ACATAGCTGG	736
115	TGCCAAGAGA	TGTCCCAGG	ACATGCCAT	CTGGGTCAC	TCCAGTGACA	GACCCCTGAC	796
117	AAAGAGCAGG	TCTCTGGAGA	CTAACGTTGCA	TGGGGCCTAG	TAACACCAAG	CCAGTGAGCC	856
119	TGTGCGTGTCA	CCGGGCCCCG	GGGGCTCCCA	GGGCTGGCA	ACTTAGTTAC	AGCTGACCAA	916
121	GGAGAAAAGTA	GTTTTGAGAT	GTGATGCCAG	TGTGCTCCAG	AAAGTGTAAAG	GGGTCTGTTT	976
123	TTCATTTCCA	TGGACATCTT	CCACAGCTTC	ACCTGACAAT	GACTGTTCT	ATGAAGAAC	1036
125	CACTTGTGTT	CTAACGAGAA	GCAACCTCTC	TCTCTTCCT	CTGTCTTTTC	CAGGCAGGGG	1096
127	CAGAGATGGG	AGAGATGTGAG	CCAAATGAC	CTTCCTGTTGG	TAAATACTGT	ATAATGCA	1156
129	GCTTTGTGCA	CAGCCCAGTG	TGGGGTTACA	GCTTTGGGAT	GACTGCTTAT	AAAGTTCTGT	1216
131	TTGCTTAGTA	TTGGCATCGT	TTTCTATAT	ACCCATAATG	CGTATAATATA	CCCATAGGGC	1276
133	TAGATCTATA	TCTTAGGGTA	GTGATGTATA	CATATACACA	TACACCTACA	TGTTGAAGGG	1336
135	CCTAACCCAGC	TTGGGAGTA	CTGACTGGTC	TCTTATCTCT	TAAAGCTAAG	TTTTTGACTG	1396
137	TGCTAATTTC	CCAAATGTGAT	CCAGTTTGTC	CTTGTAGATTA	ATAAAGACTC	GATATGAGGG	1456
139	AGGGAGGGGA	AGACCAAGCCT	CACAAATGCCG	CCACAGATGC	CTTGCTGCTG	CAGTCCTCCC	1516
141	TGATCTGTCC	ACTGAAGACA	TGAAGTCCTC	TTTTGAATGC	CAAACCCACC	ATTCAATTGGT	1576
143	GCTGACTACA	TAGAATGGGG	TTGAGAGAAAG	ATCAGTTTGG	ACTTCACATT	TTTGTGTTAA	1636
145	GTGTTAGTT	GTGTTTTTTT	GGTTTTGTTT	GTGTTGTTGT	TTGTTGTTT	TTGTTTTTG	1696
147	TTTGTGTTT	TTAAGTTCTT	GTGGGGAAAC	TTTGGGGTTA	ATCAAAGGAT	GTACTCCGT	1756
149	GGTAGACCAAG	AGGAGTAAC	AGTTTGATC	CTTGTGGGTG	TGGAAAATGT	ACCCAGGAAG	1816

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151 CTTGTGTAAG GAGGTTCTGT GACAGTGAAC ACTTTCCACT TTCTGACACC TCATCCTGCT 1876  
 153 CTACCACTCC ACCGATTCGA TTTCGATTTT TCAAATGTAG CTTGAAATTT CAATAAACTT 1936  
 155 TGCTCCTTT TCTAAAAATA AAAAAGAAAA AAAAAA 1972  
 158 (2) INFORMATION FOR SEQ ID NO: 2:  
 160 (i) SEQUENCE CHARACTERISTICS:  
 161 (A) LENGTH: 137 amino acids  
 162 (B) TYPE: amino acid  
 163 (D) TOPOLOGY: linear  
 165 (ii) MOLECULE TYPE: protein  
 167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 169 Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln  
 170 1 5 10 15  
 172 Leu His Asn Phe Ser Thr Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp  
 173 20 25 30  
 175 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val  
 176 35 40 45  
 178 Ala Leu Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His  
 179 50 55 60  
 181 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile  
 182 65 70 75 80  
 184 Arg Glu Leu Leu Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu  
 185 85 90 95  
 187 Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Arg  
 188 100 105 110  
 190 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ala Pro Glu Thr Pro Glu Thr  
 191 115 120 125  
 193 Pro Glu Ala Pro Gly Gly Ser Ala Val  
 194 130 135  
 196 (2) INFORMATION FOR SEQ ID NO: 3:  
 198 (i) SEQUENCE CHARACTERISTICS:  
 199 (A) LENGTH: 20 base pairs  
 200 (B) TYPE: nucleic acid  
 201 (C) STRANDEDNESS: single  
 202 (D) TOPOLOGY: linear  
 204 (ii) MOLECULE TYPE: cDNA  
 206 (iii) HYPOTHETICAL: NO  
 208 (iv) ANTI-SENSE: NO  
 210 (ix) FEATURE:  
 211 (A) NAME/KEY: misc\_feature  
 212 (B) LOCATION: 1..20  
 213 (D) OTHER INFORMATION:/note= "PCR forward primer"  
 215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 217 CCATCTGGGT CCACTCCAGT 20  
 219 (2) INFORMATION FOR SEQ ID NO: 4:  
 221 (i) SEQUENCE CHARACTERISTICS:  
 222 (A) LENGTH: 20 base pairs  
 223 (B) TYPE: nucleic acid  
 224 (C) STRANDEDNESS: single  
 225 (D) TOPOLOGY: linear

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227 (ii) MOLECULE TYPE: cDNA  
229 (iii) HYPOTHETICAL: NO  
231 (ix) FEATURE:  
232 (A) NAME/KEY: misc\_feature  
233 (B) LOCATION: 1..20  
234 (D) OTHER INFORMATION:/note= "PCR reverse primer"  
236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
238 AGGACAGTGG GAGTGGCACC 20  
240 (2) INFORMATION FOR SEQ ID NO: 5:  
242 (i) SEQUENCE CHARACTERISTICS:  
243 (A) LENGTH: 1946 base pairs  
244 (B) TYPE: nucleic acid  
245 (C) STRANDEDNESS: single  
246 (D) TOPOLOGY: linear  
248 (ii) MOLECULE TYPE: cDNA  
250 (iii) HYPOTHETICAL: NO  
252 (iv) ANTI-SENSE: NO  
254 (ix) FEATURE:  
255 (A) NAME/KEY: CDS  
256 (B) LOCATION: 241..642  
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
260 AATTGGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC 60  
262 AACTCCAGCT GGAGCCCTG CTTGGCTTTG GGTTTGGTCT GCAGCCCTTCC CCCCCCTCT 120  
264 AGCCTCAGGG CCGGACTCCA GCGCAGAGCC CAGCCCAGCG CAGCCTGCCA GCAGCCACCC 180  
266 AGCGGCCAGC CCGCCACGAA CCCGGCAGAGA CCTTCCCTAGC AGCCCGAGCC 240  
268 ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG 288  
269 Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln  
W--> 270 5 10 15  
272 CTG CAC AAT TTC TCC ATC TCC TTC TTC TCT TCT CTG CTT GGA GGG GAT 336  
273 Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp  
274 20 25 30  
276 GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG 384  
277 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val  
278 35 40 45  
280 GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT 432  
281 Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His  
282 50 55 60  
284 CTG ATG TAT GCT GTG AGA GAG GAG CTG GAG ATC CTG AAG GAG CAG ATC 480  
285 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile  
286 65 70 75 80  
288 CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG 528  
289 Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu  
290 85 90 95  
292 TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT 576  
293 Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys  
294 100 105 110  
296 CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC 624  
297 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala  
298 115 120 125

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/403,861A

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TIME: 15:12:03

Input Set : A:\Riccardi1.txt  
Output Set: N:\CRF3\01082001\I403861A.raw

300 CCT GGT GGT TCT CGC GTG TAA GTGGCTC TGT CCT CAGG GTGGCAGAG	672
301 Pro Gly Gly Ser Ala Val	
302 130	
304 CCACTAAACT TGT TTTACCT AGT TCT TCC AGT TTTGT TTT TGGCT CCCC AGCATCATCT	732
306 CACAGGGAGA ACT TTACACC TACCA CAGCT GGT GCAAGAAGA GAT GTCTCAA GGACATGGCC	792
308 ACCTCGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCG GTC TCTGGAG GCTGACTTGC	852
310 ATGGGGCTCA GAAACACCAA GCCAGTGAGC CTCTAAATGCT AC TCGCCCT GGGGCTCC	912
312 AGGGCTGGG CAACTTAGCT GCAACTGGCA AAGGAGAAGG GTAG TTTGAG GTC GACACC	972
314 AGTTTGCCTC AGAAAGTTA AGGGGCTGT TCTCATTC CATGGACATC TTCAACAGCT	1032
316 TCACCTGACA ACGACTGTT CTA TGAAGAA GCCACTTGTG TTTAAGCAG AGGAAACCTC	1092
318 TCTCTTCCTC TCT GTT CCGT GAAGG CAGGC GACACAGATC GGAGAGATTC ACCCAAGTCA	1152
320 GCCTTCTGTT GGTTAATATG GTATAATGCA TGCGTTGTG CACAGCCCAG TGTGGGATTA	1212
322 CAGC TTTGGG ATGACCCCTT ACAAAGTTCT GTT GGT TAG TAT TGGCATA GTT TTTCTAT	1272
324 ATAGCCATAA ATGCGTATAT ATACCCATAG GCCTAGATCT GTAT CTTAGT GTAGCGATGT	1332
326 ATACATATAA ACATCCACCT ACAT GTT GAA GGGCCTAACG AGCCTTGGGA GTATTGACTG	1392
328 GTCCCTTAC TCT TATGGCT AAGT CTT TGA CTG GTT CAT TTACCAAGTT GACCCAGTT	1452
330 GTCTTTAGG TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCC TCTGAAT	1512
332 GCGGCCACCG ATGCCCTGCT GCGCAACCC TT TCCCAGC TGTCCACTGA AAC GTGAA GT	1572
334 CCT GTT TGA ATGCCAAACC CACCA TT CAC TGGCCTGAC TACATAGAAT GGGTTGAGAG	1632
336 AAGATCAGTT TGGGCTTCAC AGT GTT CATTT GAAAAGCGT TTTTGT TTTTGAATTA	1692
338 TTGTGAAAAA CTTTCAAGTG AACAGAAGGA TG GTG CCTA CTG TGGATGA GGGATGAACA	1752
340 AGGGGATGGC TTGATCCAA TGGACCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG	1812
342 GGTTTTGTGA CAGTGAACAC TT TCCACTTT TTGACACCTT ATCCTGTATGT ATGGTTCCAG	1872
344 GATTTGGATT TTGATTTCC AAATGTAGCT TGAAATTCA ATAAACTTTG CTC TGT TTTT	1932
346 CTAAAAATAA AAAA	1946
349 (2) INFORMATION FOR SEQ ID NO: 6:	
351 (i) SEQUENCE CHARACTERISTICS:	
352 (A) LENGTH: 134 amino acids	
353 (B) TYPE: amino acid	
354 (D) TOPOLOGY: linear	
356 (ii) MOLECULE TYPE: protein	
358 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
360 Met Asn Thr Glu Met Tyr Glu Thr Pro Met Glu Val Ala Val Tyr Gln	
361 1 5 10 15	
363 Leu His Asn Phe Ser Ile Ser Phe Ser Ser Leu Leu Gly Gly Asp	
364 20 25 30	
366 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val	
367 35 40 45	
369 Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His	
370 50 55 60	
372 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile	
373 65 70 75 80	
375 Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu	
376 85 90 95	
378 Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys	
379 100 105 110	
381 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala	
382 115 120 125	
384 Pro Gly Gly Ser Ala Val	

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/403,861A DATE: 01/08/2001  
TIME: 15:12:04

Input Set : A:\Riccardi1.txt  
Output Set: N:\CRF3\01082001\I403861A.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:394 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[peptide]